```
Notch(C)    IDEC-SNP    CQNGGTC---D-VGSY-C-CPPGFT    GK---CE-N

10244(C)    -NECTM---   CQH---C     VNT-GSY-CKC-SG--     G--L-C  D
80                                  CRCFPGYT
95          VNECGMKPRP  CQHR  C     VNTHGSYKCFCLS        GKT CSQ D
                                                         GHMIMP  D
133         VNSRTCAMIN  CQYS  C     EDTEEGPQCLCPSS       GLRLAPN
175         IDECASGKVI  CPYNRRC     VNTFGSYYCKCHIGFE     LQYISGR
220         INECTMDSHT  CSHHANC     FNTQGSF CKCKQGYK     GNGRLCS

CD97(C)     V-EC-SG-Q--C-SS--C      -NTVGSY-CRCRPGW-P-PG-PN---   D

EGF(C)      NSDSECPLSHDGYCLHDGVCMYIEALDKYACNCVVGYI---GER--CQYRDLKWWELR
```

Figure 1

```
GGCTGGAGAA GAAACAGCAA GGGAGTCTGT GAAGCTACAT GCGAACCTGG
ATGTAAGTTT GGTGAGTGCG TGGGACCAAA CAAATGCAGA TGCTTTCCAG
GATACACCGG GAAAACCTGC AGTCAAGATG TGAATGAGTG TGGAATGAAA
CCCCGGCCAT GCCAACACAG ATGTGTGAAT ACACACGGAA GCTACAAGTG
CTTTTGCCTC AGTGGCCACA TGCTCATGCC AGATGCTACG TGTGTGAACT
CNAGGACATG TGCCATGATA AACTGTCAGT ATAGCTGTGA AGACACAGAA
SEQ ID NO: 1


GGCTGGAGAA GAAACAGCAA GGGAGTCTGT GAAGCTACAT GCGAACCTGG
ATGTAAGTTT GGTGAGTGCG TGGGACCAAA CAAATGCAGA TGCTTTCCAG
GATACACCGG GAAAACCTGC AGTCAAGATG TGAATGAGTG TGGAATGAAA
CCCCGGCCAT GCCAACACAG ATGTGTGAAT ACACACGGAA GCTACAAGTG
CTTTTGCCTC AGTGGCCACA TGCTCATGCC AGATGCTACG TGTGTGAACT
CNAGGACATG TGCCATGATA AACTGTCAGT ATAGCTGTGA AGACACAGAA
GAAGGGCCAC AGTGCCTGTG TCCATCCTCA GGACTCCGCC TGGCCCCAAA
TGGAAGAGAC TGTCTAGATA TTGATGAATG TGCCTCTGGT AAAGTCATCT
GTCCCTACAA TCGAAGATGT GTGANCACAT TTGGAAGCTA CTACTGCAAA
TGTCACATTG GTTTCGAACT GCAATATATC AGTGGACGAT ATGACTGTAT
AGATATAAAT GAATGTACTA TGGATAGCCA TACGTGCAGC CACCATGCCA
ATTGCTTCAA TACCCAAGGG TCCTTCAAGT GTAAATGCAA GCAGGGATAT
AAAGGCAATG GACTTCGGTG TTCTGCTATC CCTGAAAATT CTGTGAAGGA
AGTCCTCAGA GCACCTGGTA CCATCAAAGA CAGAATCAAG AAGTTGCTTG
CTCACAAAAA CAGCATGAAA AAGAAGGCAA AAATTAAAAA TGTTACCCCA
GAACCCACCA GGACTCCTAC CCCTAAGGTG AACTTGCAGC CCTTCAACTA
TGAAGAGATA GTTTCCAGAG GCGGGAACTC TCATGGAGGT AAAAAAGGGA
ATGAAGAGAA AATGAAAGAG GGGCTTGAGG ATGAGAAAAG AGAAGAGAAA
GCCCTGAAGA ATGACATAGA GGAGCGAAGC CTGCGAGGAG ATGTGTTTTT
CCCTAAGGTG AATGAAGCAG GTGAATTCGG CCTGATTCTG GTCCAAAGGA
AAGCGCTAAC TTCCAAACTG GAACATAAAG ATTTAAATAT CTCGGTTGAC
TGCAGCTTCA ATCATGGAT CTGTGACTGG AAACAGGATA GAGAAGATGA
TTTTGACTGG AATCCTGCTG ATCGAGATAA TGCTATTGGC TTCTATATGG
CAGTTCCGGC CTTGGCAGGT CACATGAAAG ACATTGGCCG ATTGAAACTT
CTCCTACCTG ACCTGCAACC CCAAAGCAAC TTCTGTTTGC TCTTTGATTA
CCGGCTGGCC GGAGACAAAG TCGGGAAACT TCGAGTGTTT GTGAAAAACA
GTAACAATGC CCTGGCATGG GAGAAGACCA CGAGTGAGGA TGAAAGTGG
AAGACAGGGA AAATTCAGTT GTATCAAGGA ACTGATGCTA CCAAAAGCAT
CATTTTTGAA GCAGAACGTG GCAAGGGCAA AACCGGCGAA ATCGCAGTGG
ATGGCGTCTT GCTTGTTTCA GGCTTATGTC CAGATAGCCT TTTATCTGTG
GANNNCTGAA TGGTACTATC TTTATATTTG ACTTTGTATG TCAGTTCCCT
GGTTTTTTTG ATATTGCATC ATAGGACCTC TGGCATTTTA AAATTACTAG
CTGAAAAATT G
SEQ ID NO: 2
```

FIGURE 2

GWRRNSKGVCEATCEPGCKFGECVGPNKCRCFPGYTGKTCSQDVNECGMKPRPCQHR
CVNTHGSYKCFCLSGHMLMPDATCVNSRTCAMINCQYSCEDTE
SEQ ID NO:3

GWRRNSKGVCEATCEPGCKFGECVGPNKCRCFPGYTGKTCSQDVNECGMKPRPCQHR
CVNTHGSYKCFCLSGHMLMPDATCVNSRTCAMINCQYSCEDTEEGPQCLCPSSGLRLAP
NGRDCLDIDECASGKVICPYNRRCVNTFGSYYCKCHIGFELQYISGRYDCIDINECTMDS
HTCSHHANCFNTQGSFKCKCKQGYKGNGLRCSAIPENSVKEVLRAPGTIKDRIKKLLAH
KNSMKKKAKIKNVTPEPTRTPTPKVNLQPFNYEEIVSRGGNSHGGKKGNEEKMKEGLE
DEKREEKALKNDIEERSLRGDVFFPKVNEAGEFGLILVQRKALTSKLEHKDLNISVDCSF
NHGICDWKQDREDDFDWNPADRDNAIGFYMAVPALAGHMKDIGRLKLLLPDLQPQSN
FCLLFDYRLAGDKVGKLRVFVKNSNNALAWEKTTSEDEKWKTGKIQLYQGTDATKSIIF
EAERGKGKTGEIAVDGVLLVSGLCPDSLLSVDDXMVLSLYLTLYVSSLVFLILHHRTSGI
LKLLAEKL
SEQ ID NO:4

FIGURE 3

ACTAGTGATTCCATCCTAATACGACTCACTATAGGGCTCGAGCGGCCGCCCGGGCAGGTCTGCAGGACAGCACCCGGTA
ACTGCGAGTGGAGCGGAGCACCCGAGCGGCTGAGGAGGAGGAGGCGGCGGCTTAGCTGCTACGGGGTCCGGCGGCGCC
CTCCCGAGGGGGGCTCAGGAGGAGGAAGGAGGACCCGTGCGAGAATGCCTCTGCCCTGGAGCCTTGCGCTCCCGCTGCTG
CTCCCCTGGGTGGCCGGAGGTGGTTCGGGAACGCGGCCAGTGCAAGGCATCACGGGTTGTTAGCATCGGCACGTCAGCCTGG
GGTCTGTCACTATGGAACTAAACTGGCCTGCTGCTGGAGGACCAAACAAATGCAGATGCTTTCCAGGATACACCGGAAAACCTGCAGT
AACCTGGATGTAAGTTTGGTGAGTGCGTGGGAGATGTGAATGACAGATGTGTGAATACACACAGATGTGAATACACACAGAGT

CAAGATGTGAATGAGTGTGAATGACAAACCCGGCCATGCCAACACAGATGTGAATACACACAGGAGTCTGTGAAGCTACATGCG
TTGCCTCAGTGCCCACATGCTCATGCCAGATGCTACGTGTGTGAACTCTAGACATGTGCCATGATAAACTGTCAGTATA
GCTGTGAAGACACAGAAGAGGGCCACAGTGCCTGTCCTGTGTCCATCCTCAGGACTCCGCCTGGCCCCAAATGGAAGAGACTGT
CTAGATATTGATGAATGCTCCTCTGGTAAGTGCATAATCAGTGGACGATATGACTGTATAGATATAAATGAATGTACTACTA
CTGCAAATGTCACATTGGTTTCGAACTGCCAATGCCACCATGCCTGTGTTCTGTAAAGTCATCTGTCCCCTACAATCGAAGATGTGTGAACACATTTGAAGCTACTA
ATAGCCATACGTGCAGCCACCATGCCAATTGCTTCAATACCCAAGGGTCCTTCAAGTGTAAATGCAAGCAGGGATATAAA
GGCAATGGACTTCGGTGTTCTCTATCCTGAAAATTCTGTGAAGGAAGTCCTCAGAGCACACCTGGTACCATCAAAGACAG
AATCAAGAAGTGCTTGCTCACAAAACAGCATGAAAAATTAAAAATGTTACCCCAGAACCCACCAGA
CTCCTACCCCTAAGGTGAACTTGCAGCCCTTCAACTATGAAAGAGATAGTTTCCAGAGGCGGAACTCTCATGGAGTAAA
AAAGGGAATGAAAGAGAGAAATGAAAGAAGAGGGCTTGAGGATGAAGAGAAAGAAAGCCCTGAAGAATGACWTAGAGGA
GCGAAGCCTGCGAGGAGATGTGTTTTCCTAAGGTGAATGAAGCAGGTGAATTCGGCCTGATTCTGGTCCAAGGAAAG
CGTAACTTCCAAACTGAACATGAAGATTTAAATATCTCGGTTGACTGCAGCTTCAATCATGGCATCGTGACTGACTGGAAA
CAGGATAGAGAAGATGATTTTGACTGGAATCCTGAATCCGATTGAAACTTCTCTCCTACCTGCAACCCCAAAGCAACTTCTGTTTGCTCT
GGCAGGTCACAGAAAGACATTGGCCGATTGGGAGACAAAGTCGGGAGAACTTCGGGAAACTTCGTGAAAAACAGTAACATGCCCTGGCATGGGAG
TTGATTACCGGCTGGCCGGAGACAAAGTCGGGAAGACAGGGAAATTCAGTTGTATCAAGAACTGATGCTACCAAAAGCATCAT
AAGACCACGAGTGAGATGAAAGTGAAGACAGAGGGAAATTCAGTTGTATCAAGAACTGATGCTACCAAAAGCATCAT
TTTGAAGCAGAACGTGGCAAGGGCAAAACCGGCAAAATCGCAGTGGATGGCGTCTTGCTTGTTGTTTCAGCTTATGTCCAG
ATAGCCTTTTATCTGTGATGACTGAATGTTACTATCTTTATATTTGACTTTGTATGTCAGTTCCGTGTTTTTTGATA
TTGSATCATAGGACCTCTGGCATTTTAAAATTACTAAGCTGAAAAATTGTAATGTACCAACAGAAATTATTATTGTAAGA
TGCCTTTMTTGTATAAGATATGCCAATATTGCTTTAAATATCATATCACTGTATCTTCTCAGTCATTTCTGAATCTTTC
CACATTATATTATAAAATATGAAAATGTCAGTTTATCTCCCCTCCTCAGTATATCTGATTTGTATAAGTAAGTTGATGA
GCTTCTCTCTGCAACATTTCTAGAAAATAGAHAAAAAGCACAGAGAAATGTTTAACTGTTTGACTCTTTATGATAGTTTT
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TCTTTGTAATAATATCCAAATCATCAAAAAAAAAAAAAAA
SEQ ID NO:5

MPLPWSLALPLLLPWVAGGFGNAASARHHGLLASARQPGVCHYGTKLACCYGWRRNSKGVCEATCEPGCKFGECVGPNKC
RCFPGYTGKTCSQDVNECGMKPRPCQHRCVNTHGSYKFCFCLSGHMLMPDATCVNSRTCAMINCQYSCEDTEEGPQCLCPS
SGLRLAPNGRDCLDIDECASGKVICPYNRRCVNTFGSYYCKCHIGFELQYISGRYDCIDINECTMDSHTCSHHANCFNTQ
GSFKCKCKQGYKGNGLRCSAIPENSVKEVLRAPGTIKDRIKKLLAHKNSMKKKAKIKNVTPEPTRTPTPKVNLQPFNYEE
IVSRGGNSHGGKKGNEEKMKEGLEDEKREEKALKNDXEERSLRGDVFFPKVNEAGEFGLILVQRKALTSKLEHKDLNISV
DCSFNHGICDWKQDREDDFDWNPADRDNAIGFYMAVPALAGHKDIGRLKLLLPDLQPQSNFCLLFDYRLAGDKVGKLRV
FVKNSNNALAWEKTTSEDEKMKTGKIQLYQGTDATKSIIFEAAERGKGKTGEIAVDGVLLVSGLCPDSLLSVDD
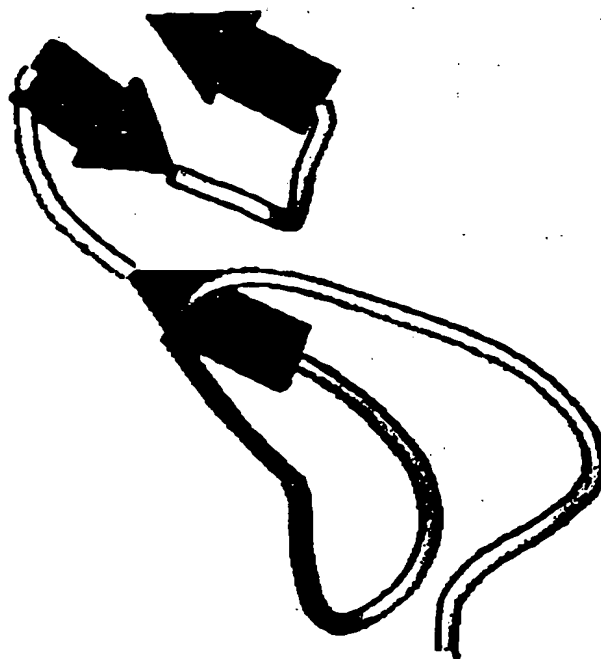SEQ ID NO: 6

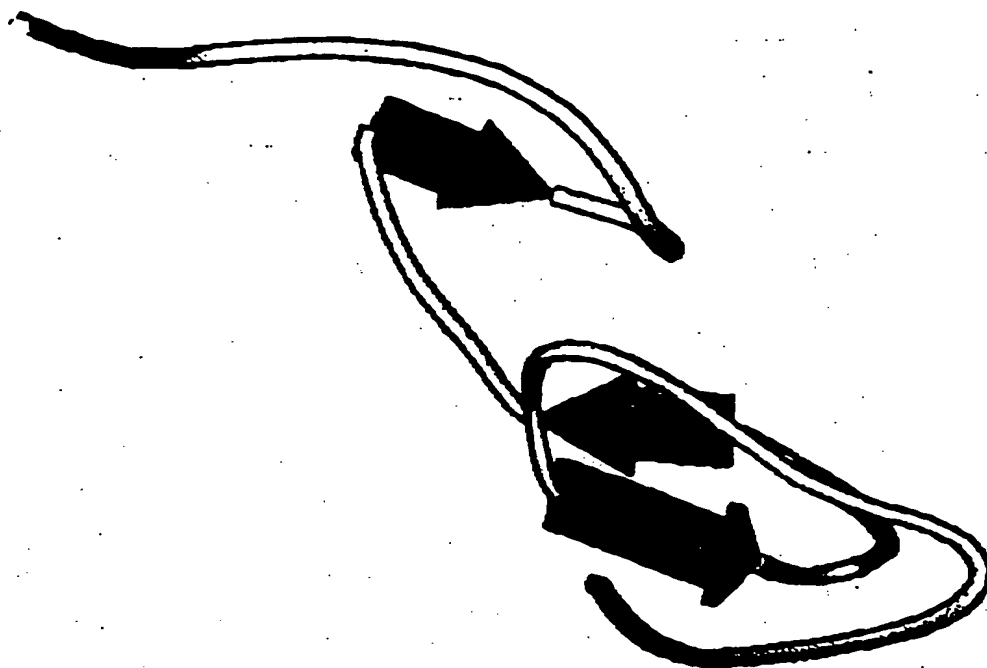FIGURE 4

EGFL6 (221-260 aa)
3D Model

EGF
NMR Structure

Figure 5